

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
- (ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CERRONE, MICHAEL C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0527 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSTUT10
(B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	
				5					10					15	
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	
				20					25					30	
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu	
				35					40					45	
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu	
				50					55					60	
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	
				65					70					75	
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	
				80					85					90	
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	
				95					100					105	
Phe	Glu	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
				110					115					120	
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln	
				125					130					135	
Leu	Cys	Arg	Tyr	Pro	Asp										
				140											

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val	
				5					10					15	
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe	
				20					25					30	
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met	
				35					40					45	
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met	
				50					55					60	
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val	
				65					70					75	
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met	
				80					85					90	
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro	
				95					100					105	
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg	
				110					115					120	
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp	
				125					130					135	
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val	
				140					145					150	
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asp	Asn	Tyr	Phe	Tyr	Ile	

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His Ser Ile Trp	155	His Met Leu Ile Ala	160	Gly Ser Val Gly Phe	165
Leu Pro Pro Arg	170	Ala Lys Thr Asp His	175	Gly Val Pro Ser Gly	180
Arg Ala Arg Gly	185	Cys Gly Tyr Gln Leu	190	Cys Ile Asn Glu Gln	195
Glu Pro Gly Pro	200	Arg Gly Pro Arg Arg	205	Gly His Cys Gln Gln	210
Leu Cys Gln Leu	215	Arg Gly Ala Leu Gly	220	Leu Ala Leu Arg Gly	225
Glu Cys Phe Leu	230	Gly Phe Phe Leu Gly	235	Val Trp Ser Pro Leu	240
Arg Arg Gln Ala	245	Val Phe Leu Glu Asp	250	Met Glu Ser Phe Ser	255
Thr Gln Asn Ser	260	Ser Arg Asp Leu Glu	265	Glu Ser Phe Ser Arg	270
Glu Leu Pro Glu	275	Ser Arg Asp Leu Glu	280	Pro Phe Pro Gly His	285
Leu Arg Thr Gly	290	Gly Leu Glu Ser Pro	295	Cys Ile Met Glu Ser	300
Glu Ser Leu Leu	305	Ala Tyr Ala Gly Thr	310	Glu Ser Leu Arg Thr	315
Ser Gln Asp Met	320	Gln Val Trp Ser Leu	325	Ser Trp Asp Ala Glu	330
Ser Thr Ala Ser	335	Asp Ser Phe Pro Gly	340	Arg Gln Ser Pro Val	345
Gln Ile Ser Arg	350	Phe Gln Arg Arg Trp	355	Ser Leu Ser Trp Gly	360
Leu Pro Ser Gln	365	Ser Ser Gln Arg Leu	370	Ser Asn Ser Gly Leu	375
Arg Asp Cys Arg	380	Met Asp Gly Ala Gly	385	Thr Gly Ala Val Trp	390
Ala Gly Ile Leu	395		400		405
	410				

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

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CAAGTATAGG AGATTTCCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG 60
ATTACTAAGT TTTTCTTTCG CTATGGTCCA TGTTGCCTAC AGCCTCTGCT TACCGATGAG 120
AAGGTCAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTTTCATG CAAATATTGA 180
AAACTCTTGG AATGAGGAAG AAGTTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT 240
GAGCCTTGGC TTA CTTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT 300
AAACTGGAGA GAATTCAGTT TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG 360
TACTTTCCAT GTTTTAATTT ATGGATGGAA ACGAGCTTTT GAGGAAGAGT ACTACAGATT 420
TTATACACCA CCAAACCTTG TTCTTGCTCT TGT TTTGCCC TCAATTGTAA TTCTGGATCT 480

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TTTGCAGCTT TGCAGATACC CAGACTGAGC TGGAAGCTGGA ATTTGTCTTC CTATTGACTC 540
TACTTCTTTA AAAGCGGCTG CCCATTACAT TCCTCAGCTG TCCTTGCACTG TAGGTGTACA 600
TGTGACTGAG TGTTGGCCAG TGAGATGAAG TCTCCTCAAA GGAAGGCAGC ATGTGTCCCTT 660
TTTCATCCCT TCATCTTGCT GCTGGGATTG TGGATATAAC AGGAGCCCTG GCAGCTGTCT 720
CCAGAGGATC AAAGCCACAC CCAAAGAGTA AGGCAGATTA GAGACCAGAA AGACCTTGAC 780
TACTTCCCTA CTTCCACTGC TTTTTCCTGC ATTTAAGCCA TTGTAAATCT GGGTGTGTTA 840
CATGAAGTGA AAATTAATTC TTTCTGCCCT TCAGTTCTTT ATCCTGATAC CATTTAACAC 900
TGTCTGAATT AACTAGACTG CAATAATTCT TTCTTTTGAA AGCTTTTAAA GGATAATGTG 960
CAATTCACAT TAAAATTGAT TTTCCATTGT CAATTAGTTA TACTCATTTT CCTGCCTTGA 1020
TCTTTCATTA GATATTTTGT ATCTGCTTGG AATATATTAT CTTCTTTTAA ACTGTGTAAT 1080
TGGTAATTAC TAAAACTCTG TAATCTCCAA AATATTGCTA TCAAATTACA CACCATGTTT 1140
TCTATCATTC TCATAGATCT GCCTTATAAA CATTTAAATA AAAAGTACTA TTTAATGATT 1200
TAAAAAATAA AAA 1213

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGCGTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCCCTGGCC 60
ATTCGGAGTC GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCATGTT CTTCTCCACG 120
TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTTCT GCATCATGGA CTACGATGTG 180
CTGCAGTTCT GTGATTTCCT GGGCTCCTTA ATGTCCGTGT GGGTCACTGT CATTGCCATG 240
GCTCGTTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTTGC TGGGAGCTAT GCTGCTGTCC 300
ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTTCGCC 360
CTGGGGATCT TGGCCACAGC CTGGACAGTA CGCAGCGTCC GCCGCCGGCA CTGCTACCCA 420
CCCACGTGGC GCCGCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGC AGGCAGTGCC 480
GTCCTGCTTT ATGCTTTTGT GGAGACCCGG GACAACTACT TCTACATTCA CAGCATTTGG 540
CATATGCTCA TTGCGGGCAG TGTGGGCTTC CTGCTGCCCC CTCGTGCCAA GACTGACCAC 600
GGGTCCCAT CTGGAGCCCG GGCCCGGGGC TGTTGGTTACC AGCTATGCAT CAACGAGCAG 660
GAGGAGCCTG GGCTCTGTGG GCCCAGGAGG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720
AGAGGGGCTT TGGGCCTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTTCTGGGG 780
GTGTGGAGCC CTCTTAGAAG GAGACAGGCT GTATTTCTTG AGGACATGGA GTCTTTCTCA 840
AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCCAG GACATGGAGA ACTTCCTGAG 900
GGCCTGGAGT CCCCTGTCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960
GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGTGGA GCCTTTCTCT GGATGCAGAG 1020
CCTTCCCAAG ACATGGATT CTTCCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080
TTCCAGAGGA GGTGGAGTCT ATCTTGGGGA AACCATAATT CCAGATTTTC CCAGAGGCTC 1140
AGCAACTCTG GCCTCAGGCT TCCTTCCCAG AGGCAGCGTC TGGGCTGTGC TGTGCTGTGG 1200
AGGAGGGATT GCAGGATGGA TGGAGCTGGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260
GTTTGATACA GGTGGAGTCT CTGTGTCTCC ATAGAAG 1297

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 1216498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Gly	Arg	Ala	Met	Val	Val	Arg	Leu	Gly	Leu	Gly	Leu	Leu	Leu
				5					10					15
Leu	Ala	Leu	Leu	Leu	Pro	Thr	Gln	Ile	Tyr	Cys	Asn	Gln	Thr	Ser
				20					25					30
Val	Ala	Pro	Phe	Ser	Gly	Asn	Gln	Ser	Ile	Ser	Ala	Ala	Pro	Asn
				35					40					45
Pro	Thr	Asn	Ala	Thr	Thr	Arg	Ser	Gly	Cys	Ser	Ser	Leu	Gln	Ser
				50					55					60
Thr	Ala	Gly	Leu	Leu	Ala	Leu	Ser	Leu	Ser	Leu	Leu	His	Leu	Tyr
				65					70					75
Cys														

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 130989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Trp	Val	Pro	Val	Val	Phe	Leu	Thr	Leu	Ser	Val	Thr	Trp	Ile
				5					10					15
Gly	Ala	Ala	Pro	Leu	Ile	Leu	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu
				20					25					30
Cys	Glu	Lys	His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg
				35					40					45
Gly	Arg	Ala	Val	Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val
				50					55					60
Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu
				65					70					75
Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe
				80					85					90
Gln	Val	Ser	His	Ser	Phe	Pro	His	Pro	Leu	Tyr	Asp	Met	Ser	Leu
				95					100					105
Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	Gly	Asp	Asp	Ser	Ser	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Ala
				125					130					135
Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu	Pro	Ala	Leu	Gly	Thr
				140					145					150
Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu	Pro	Glu	Glu	Phe
				155					160					165
Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His	Val	Ile	Ser
				170					175					180
Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr	Lys	Phe
				185					190					195

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Met	Leu	Cys	Ala	Gly	Arg	Trp	Thr	Gly	Gly	Lys	Ser	Thr	Cys	Ser
				200					205					210
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Val	Leu	Gln	Gly
				215					220					225
Ile	Thr	Ser	Trp	Gly	Ser	Glu	Pro	Cys	Ala	Leu	Pro	Glu	Arg	Pro
				230					235					240
Ser	Leu	Tyr	Thr	Lys	Val	Val	His	Tyr	Arg	Lys	Trp	Ile	Lys	Asp
				245					250					255
Thr	Ile	Val	Ala	Asn	Pro									
				260										

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Leu	Ala	Cys	Leu	Cys	Cys	Lys	Lys	Gly	Gly	Ile	Gly	Phe	Lys
				5					10					15
Glu	Phe	Glu	Asn	Ala	Glu	Gly	Asp	Glu	Tyr	Val	Ala	Asp	Phe	Ser
				20					25					30
Glu	Gln	Gly	Ser	Pro	Ala	Ala	Ala	Ala	Gln	Thr	Gly	Pro	Asp	Val
				35					40					45
Tyr	Val	Leu	Pro	Leu	Thr	Glu	Val	Ser	Leu	Pro	Met	Ala	Lys	Gln
				50					55					60
Pro	Gly	Arg	Ser	Val	Gln	Leu	Leu	Lys	Ser	Thr	Asp	Leu	Gly	Arg
				65					70					75
His	Ser	Leu	Leu	Tyr	Leu	Lys	Glu	Ile	Gly	His	Gly	Trp	Phe	Gly
				80					85					90
Lys	Val	Phe	Leu	Gly	Glu	Val	His	Ser	Gly	Val	Ser	Gly	Thr	Gln
				95					100					105
Val	Val	Val	Lys	Glu	Leu	Lys	Val	Ser	Ala	Ser	Val	Gln	Glu	Gln
				110					115					120
Met	Gln	Phe	Leu	Glu	Ala	Gln	Pro	Tyr	Arg	Ala	Leu	Gln	His	
				125					130					135
Ser	Asn	Leu	Leu	Gln	Cys	Leu	Ala	Gln	Cys	Ala	Glu	Val	Thr	Pro
				140					145					150
Tyr	Leu	Leu	Val	Met	Glu	Phe	Cys	Pro	Leu	Gly	Asp	Leu	Lys	Gly
				155					160					165
Tyr	Leu	Arg	Ser	Cys	Arg	Val	Thr	Glu	Ser	Met	Ala	Pro	Asp	Pro
				170					175					180
Leu	Thr	Leu	Gln	Arg	Met	Ala	Cys	Glu	Val	Ala	Cys	Gly	Val	Leu
				185					190					195
His	Leu	His	Arg	His	Asn	Tyr	Val	His	Ser	Asp	Leu	Ala	Leu	Arg
				200					205					210
Asn	Cys	Leu	Leu	Thr	Ala	Asp	Leu	Thr	Val	Lys	Val	Gly	Asp	Tyr
				215					220					225
Gly	Leu	Ser	His	Cys	Lys	Tyr	Arg	Glu	Asp	Tyr	Leu	Val	Thr	Ala
				230					235					240
Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg	Trp	Ile	Ala	Pro	Glu	Leu	Val

	245		250		255
Asp Glu Val His	Gly Asn Leu Leu Val	Val Asp Gln Thr Lys	Ser		
	260		265		270
Ser Asn Val Trp	Ser Leu Gly Val Thr	Ile Trp Glu Leu Phe	Glu		
	275		280		285
Leu Gly Ala Gln	Pro Tyr Pro Gln His	Ser Asp Arg Gln Val	Leu		
	290		295		300
Ala Tyr Ala Val	Arg Glu Gln Gln Leu	Lys Leu Pro Lys Pro	Gln		
	305		310		315
Leu Gln Leu Ala	Leu Ser Asp Arg Trp	Tyr Glu Val Met Gln	Phe		
	320		325		330
Cys Trp Leu Gln	Pro Glu Gln Arg Pro	Thr Ala Glu Glu Val	His		
	335		340		345
Leu Leu Leu Ser	Tyr Leu Cys Ala Lys	Gly Thr Thr Glu Leu	Glu		
	350		355		360
Glu Glu Phe Glu	Arg Arg Trp Arg Ser	Leu Arg Pro Gly Gly	Ser		
	365		370		375
Thr Gly Leu Gly	Ser Gly Ser Ala Ala	Pro Ala Ala Ala Thr	Ala		
	380		385		390
Ala Ser Ala Glu	Leu Thr Ala Ala Ser	Ser Phe Pro Leu Leu	Glu		
	395		400		405
Arg Phe Thr Ser	Asp Gly Phe His Val	Asp Ser Asp Asp Val	Leu		
	410		415		420
Thr Val Thr Glu	Thr Ser His Gly Leu	Asn Phe Glu Tyr Lys	Trp		
	425		430		435
Glu Ala Gly Cys	Gly Ala Glu Glu Tyr	Pro Pro Ser Gly Ala	Ala		
	440		445		450
Ser Ser Pro Gly	Ser Ala Ala Arg Leu	Gln Glu Leu Cys Ala	Pro		
	455		460		465
Asp Ser Ser Pro	Pro Gly Val Val Pro	Val Leu Ser Ala His	Ser		
	470		475		480
Pro Ser Val Gly	Ser Glu Tyr Phe Ile	Arg Leu Glu Gly Ala	Val		
	485		490		495
Pro Ala Ala Gly	His Asp Pro Asp Cys	Ala Gly Cys Ala Pro	Ser		
	500		505		510
Pro Gln Ala Val	Thr Asp Gln Asp Asn	Asn Ser Glu Glu Ser	Thr		
	515		520		525
Val Ala Ser Leu	Ala Met Glu Pro Leu	Leu Gly His Ala Pro	Pro		
	530		535		540
Thr Glu Gly Leu	Trp Gly Pro Cys Asp	His His Ser His Arg	Arg		
	545		550		555
Gln Gly Ser Pro	Cys Pro Ser Arg Ser	Pro Ser Pro Gly Thr	Pro		
	560		565		570
Met Leu Pro Ala	Glu Asp Ile Asp Trp	Gly Val Ala Thr Phe	Cys		
	575		580		585
Pro Pro Phe Phe	Asp Asp Pro Leu Gly	Ala Ser Pro Ser Gly	Ser		
	590		595		600
Pro Gly Ala Gln	Pro Ser Pro Ser Asp	Glu Glu Pro Glu Glu	Gly		
	605		610		615
Lys Val Gly Leu	Ala Ala Gln Cys Gly	His Trp Ser Ser Asn	Met		
	620		625		630
Ser Ala Asn Asn	Asn Ser Ala Ser Arg	Asp Pro Glu Ser Trp	Asp		
	635		640		645
Pro Gly Tyr Val	Ser Ser Phe Thr Asp	Ser Tyr Arg Asp Asp	Cys		
	650		655		660
Ser Ser Leu Glu	Gln Thr Pro Arg Ala	Ser Pro Glu Val Gly	His		
	665		670		675
Leu Leu Ser Gln	Glu Asp Pro Arg Asp	Phe Leu Pro Gly Leu	Val		
	680		685		690
Ala Val Ser Pro	Gly Gln Glu Pro Ser	Arg Pro Phe Asn Leu	Leu		
	695		700		705

a) α = 0.05		b) α = 0.01		c) α = 0.001	
Test	Power	Test	Power	Test	Power
W	0.85	W	0.95	W	0.99
L	0.82	L	0.92	L	0.98
F	0.80	F	0.90	F	0.97
G	0.78	G	0.88	G	0.96
H	0.75	H	0.85	H	0.95
I	0.72	I	0.82	I	0.92
J	0.70	J	0.80	J	0.90
K	0.68	K	0.78	K	0.88
L	0.65	L	0.75	L	0.85
M	0.62	M	0.72	M	0.82
N	0.60	N	0.70	N	0.80
O	0.58	O	0.68	O	0.78
P	0.55	P	0.65	P	0.75
Q	0.52	Q	0.62	Q	0.72
R	0.50	R	0.60	R	0.70
S	0.48	S	0.58	S	0.68
T	0.45	T	0.55	T	0.65
U	0.42	U	0.52	U	0.62
V	0.40	V	0.50	V	0.60
W	0.38	W	0.48	W	0.58
X	0.35	X	0.45	X	0.55
Y	0.32	Y	0.42	Y	0.52
Z	0.30	Z	0.40	Z	0.50

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	1160		1165		1170
Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr Val Tyr Leu					
	1175		1180		1185
Phe Asp Gln Glu Ser Pro Thr Arg Glu Thr Gly Glu Pro Phe Pro					
	1190		1195		1200
Ser Thr Lys Glu Ser Leu Pro Thr Phe Leu Glu Gly Gly Pro Ser					
	1205		1210		1215
Ser Pro Ser Ala Thr Gly Leu Pro Leu Arg Ala Gly His Ser Pro					
	1220		1225		1230
Asp Ser Ser Ala Pro Glu Pro Gly Ser Arg Phe Glu Trp Asp Gly					
	1235		1240		1245
Asp Phe Pro Leu Val Pro Gly Lys Ala Ala Leu Val Thr Glu Leu					
	1250		1255		1260
Asp Pro Ala Asp Pro Val Leu Ala Ala Pro Pro Thr Pro Ala Ala					
	1265		1270		1275
Pro Phe Ser Arg Phe Thr Val Ser Pro Thr Pro Ala Ser Arg Phe					
	1280		1285		1290
Ser Ile Thr His Ile Ser Asp Ser Asp Ala Gln Ser Val Gly Gly					
	1295		1300		1305
Pro Ala Ala Gly Ala Gly Gly Arg Tyr Thr Glu Ala					
	1310		1315		